Serial No. 09/374,967
Group Art Unit: 1638

REMARKS

Reconsideration of the present application is respectfully requested. Claims 1, 3-5, 7-13, 23, 24, 32, 33, and 41-45 are pending.

Claims 5, 23, 32 and 45, have been amended. Support for the amendments is found in the original claims. Claim 1 has been cancelled and rewritten as new claim 77. New claims 78-81 have been added. Support for the new claims is found in the claims as originally filed. No new matter has been added by way of these amendments.

Claims 1, 3, 4, 7, 8, 11, 13, 24, and 33 have been cancelled without prejudice.

The marked up version of the claim amendments is found on a separate sheet attached to this amendment and titled "Version with Markings to Show Changes." It is respectfully requested that the amendments be entered.

Claim Objections

Claim 11 is objected to for improper format. The Examiner points out there should be a colon after the word "of" in line 2. Claim 11 has been cancelled without prejudice.

Rejections under 35 U.S.C. §101

Claim 45 is rejected under 35 U.S.C. §101 as directed to non-statutory subject matter.

The Examiner states: "Claim 45, as written, do [sic] not sufficiently distinguish over seeds as they exist in nature.... It is suggested that the claims be modified to refer to the hand of the inventor, *e.g.* by indicating that the seeds have the nucleotide sequence stably incorporated into their genome...."

Claim 45 has been amended to recite: "The *transformed* seed of the plant of claim 32." Support for the amendment is found in original claim 32 which recites: "A transformed plant having stably incorporated into its genome at least one nucleotide

sequence encoding a GDP-mannose pyrophosphorylase...." Seeds are inherent in plants.

It is believed the amendment obviates the rejection of Claim 45.

Rejections under 35 USC §112, first paragraph:

Claims 1, 3-5, 7-13, 23-24, 32-33, and 41-45 are rejected under 35 U.S.C. §112, first paragraph, because the specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention commensurate in scope with these claims.

Claims 1, 3, 4, 7, 8, 11, 13, 24, and 33 have been cancelled. Claim 1 has been re-written as new claim 77. Claims 5, 23, 32, and 45 have been amended.

The Examiner states: "The claims are broadly drawn to a multitude of nucleic acids that encode maize or legume GDP-mannose pyrophosphorylase, that encode SEQ ID NO:2, that have 90% identity to SEQ ID NO:1, or that encode an 'antisense RNA' of one of those nucleic acids, and plants transformed with those nucleic acids in sense or antisense orientation.... The instant specification however, only provides guidance for random sequencing of a maize cDNA library and comparison of the sequences to sequence databases to identify a clone (SEQ ID NO:1, which encodes SEQ ID NO:2) with homology to *Saccharomyces cerevisae* VIG9 GDP-mannose pyrophosphorylase (example 1) and general guidance for transformation of maize (example 2)."

Claim 1 has been cancelled and rewritten as new independent Claim 77 and dependent claims 78-81. New claim 77 reads:

"An isolated nucleotide sequence selecting from the group consisting of:

a) a nucleotide sequence encoding a maize polypeptide having GDP-mannose pyrophosphorylase activity;

b) a nucleotide sequence encoding the amino acid sequence of SEQ ID NO:2;

c) a nucleotide sequence set forth in SEQ ID NO:1; and

d) a nucleotide sequence having at least 90% identity to a nucleotide sequence of a), b), or c) having GDP-mannose pyrophosphorylase activity."

While new claims 77-81 do recite the use of various sequences that upon expression, modulate GDP-mannose pyrophosphorylase activity, this factor does not contribute to a lack of enablement. In fact, in contrast to the view of the Office Action, the present specification provides sufficient guidance for one skilled in the art to make and use the claimed sequences.

First, the Examiner appears to assert that the present specification does not provide sufficient guidance to make and use the sequences recited in claim new claim 77. This assumption is incorrect. GDP-mannose pyrophosphorylase polypeptides were known in the art prior to the present invention. In fact, guidance has been provide throughout the specification as to the various GDP-mannose pyrophosphorylase sequences that were known in the art and, moreover, the art was apprised of the functional/structural relationship of members of the enzyme class. See, page 17, lines 29-30 and page 18, lines 22-24 of the specification. Consequently, one of skill in the art would be well apprised of how to make and use sequences encompassed by independent claim 77.

In addition, guidance for determining percent sequence homology to SEQ ID NO:1 recited in independent claim 77 is provided in the specification. See, for example, page 12, lines 14-29. Generating such sequences are routine.

And finally, descriptions of phenotypic or enzymatic changes resulting from GDP-mannose pyrophosphorylase activity can be found on page 3, lines 1-3. Szumilo *et al.* and Hashimoto *et al.* referenced on pages 17 and 18, respectively, apply similar assays to functionally characterize members of the GDP-mannose pyrophosphorylase family. Consequently, methods for assaying GDP-mannose pyrophosphorylase activity is routine in the art.

Thus, a rational scheme for identifying sequences encompassed by independent claim 77 has been provided in the specification. The skilled artisan could choose among possible modifications to produce sequences within the parameters set forth in the claims and then test these modified variants to determine if, upon expression, GDP-mannose pyrophosphorylase activity is present. Although some quantity of experimentation would be required, the level of experimentation would not be undue in view of the amount of direction provided in the specification, the state of the art, and the level of skill of one in the art. These factors all favor a conclusion that one of skill in the art could practice the claimed invention without undue experimentation.

The Examiner states: "The instant specification, fails to provide guidance for the isolation of [sic] construction of nucleic acids that encode legume GDP-mannose pyrophosphorylases, ... and plants transformed with those nucleic acids in a sense or antisense orientation."

References to legume GDP- mannose pyrophosphorylase have been cancelled without prejudice.

The Examiner further states: "The instant specification fails to provide guidance for the exact hybridization or amplification conditions and probes/primers to use in isolation of nucleic acids other than SEQ ID NO:1."

As cited previously, the specification provides such guidance beginning on page 9, line 3 (generation of primers), page 10, beginning on line 1 (generation and use of probes), and page 10, line 23 to page 12, line 18 (hybridization conditions) and generating variants of a sequence by such means is routine in the art.

The Examiner states: " The specification .... suggests making conservative substitutions in SEQ ID NO:2 to make nucleic acid [sic] that encode variants. However making 'conservative' substitutions .... does not provide predictable results."

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In support of the 35 U.S.C. 112, first paragraph, rejection, the Examiner cites Lazar *et al.* who teach that a conservative substitution reduced biological function while "nonconservative" substitutions had no effect.

Likewise, the Examiner cites Hill *et al.* who teach that ADP-glucose pyrophosphorylase proteins mutated to substitute arginine for histidine (a "conservative" substitution), reduced the enzymes activity.

The Examiner concludes: "The nucleic acids encoding all these mutated proteins however, would hybridize under high stringency conditions to the nucleic acids encoding the original protein ... Given the claim breath [sic], unpredictability, and lack of guidance as discussed above, undue experimentation would have been required by one of skill in the art to develop and evaluate nucleic acids with 90% identity to SEQ ID NO:1 ... not all of these nucleic acids will encode a functional protein. The specification does not teach how to use nucleic acids that do not encode a functional protein."

Present claim 77 recites: "... a nucleotide sequence encoding a maize polypeptide *having GDP-mannose pyrophosphorylase activity*...." It is respectfully pointed out that non-operative embodiments are not claimed. Only those variants *having GDP-mannose pyrophosphorylase activity* are claimed.

The specification clearly states beginning on page 7, line 30: "Guidance as to appropriate amino acid substitutions *that do not affect biological activity* of the protein of interest may be found in the model of Dayhoff et al. (1978) Atlas of Protein Sequence and Structure (Natl. Biomed. Res. Found., Washington, D.C.), herein incorporated by reference. Conservative substitutions, such as exchanging one amino acid with another having similar properties, *may* be preferred." (italics inserted). The disclosure plainly acknowledges that conservative substitutions per se, *may* not produce a functional protein, but is one of many tools the skilled artisan may use to produce a nucleic acid of the currently claimed invention.

The screening of a group of sequences containing from a few to many, inoperative species in order to isolate one or more operative species is a common

practice in many aspects of the biotechnological arts. With the guidance provided in the specification as cited herein and in the previous responses, isolation of operative embodiments from a group of candidate sequences as claimed in present independent claim 77, clearly has a reasonable expectation of success by one skilled in the art.

The case applying the undue experimentation standard is In re Wands where the court held that "the test is not merely quantitative, since *a considerable amount of experimentation is permissible*, if it is merely routine, or if the specification in question provides a reasonable amount of guidance with respect to the direction in which the experimentation should proceed." 8 U.S.P.Q.2d 1400, 1404 (Fed. Cir. 1988) [italics added]. In rejecting the Patent Office's position that because only 2.8% of the cell lines tested fell within the scope of the claim and that the isolation of inventive cell lines was unpredictable, the court emphasized that the skilled artisan, guided by the specification, could, nonetheless, reasonably expect to achieve antibodies commensurate with the scope of the claims.

As stated herein, one skilled in the art would reasonably expect that those nucleic acid molecules that have at least 90% identity to SEQ ID NO:1, and possess GDP-mannose pyrophosphorylase activity could be used in the presently claimed invention. Methods for determining percent identities are well known and routine in the art and have been cited previously. Testing for GDP-mannose pyrophosphorylase activity is also well known and cited on page 17 of the specification beginning on line 28.

The Examiner asserts the specification is non-enabling for plants transformed with GDP-mannose pyrophosphorylase DNA in an antisense orientation. The Examiner cites Keller, et al, as evidence of the unpredictability of the art.

As noted above, screening transformants for a desired phenotype is an integral aspect of the biotechnological arts. Kellar *et al.*, on page 133, column 1, second paragraph states that the plants in figure 2 (b, c,) were *selected* on the basis of Northern blots to have "significantly reduced" transcripts in comparison to the

wild-type plants. It is not reported what phenotype plants with *intermediate* levels of reduced GDP-mannose pyrophosphorylase activity exhibited. Kellar *et al.* therefore does not teach unpredictability in the use of antisense constructs, merely that transforming plants with antisense DNA can yield a population of plants with transcription sufficiently down-regulated that the effects of such down- regulation may be studied.

However, to further prosecution and not to limit the scope of the claimed invention, new claim 77 has been written to remove reference to nucleic acids encoding an antisense RNA.

The Examiner states: "... the specification fails to describe sequence motifs critical for enzymatic function or how to assay for GDP-mannose pyrophosphorylase activity.....and does not describe the exact hybridization conditions and PCR primers needs [sic] to isolate the claimed nucleic acids."

The Examiner's concern that the specification does not recite exact hybridization conditions, specific PCR needed, critical sequence motifs, and functional assays is either incorrect or unwarranted.

All of the above parameters can be found in the specification or were well known or routine in the art at the time the application was filed.

Conserved motifs were known in the art at the time of filing: see Hashimoto, et al, page 16311, top of column 2. Assays to test for the function of GDP-mannose pyrophosphorylase activity are found on beginning on page 17, line 28 to page 18, lines 1-3. Hybridization conditions are given beginning on page 11, line 3 through page 12, line 13. Methods of designing primers and isolation via PCR besides being well known in the art at the time of filing (see citations in specification) are detailed on page 9, lines 3-16.

In light of the above remarks, it is submitted that the present specification enables one of ordinary kill in the art to make and use the claimed invention without undue experimentation.

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Possession:

Claims 1, 3-5, 7-13, 23-24, 32-33, and 41-45 are rejected under 35 USC §112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The Examiner states: "... the specification only describes a coding sequence from maize that comprises SEQ ID NO:1. Applicant does not describe other nucleic acids encompassed by the claims, including those from legumes or that encode other maize GDP-mannose pyrophosphorylases, and the structural features that distinguish all such nucleic acids from other nucleic acids are not provided."

The Examiner further states: "The claims include no description the protein [sic] encoded by nucleic acids that have 90% identity to SEQ ID NO:1."

Claims 1, 3, 4, 7, 8, 11, 13, 24, and 33 have been cancelled without prejudice, and claims 5, 23, 32, and 45 amended. Claim 1 has been rewritten as new claim 77 which reads:

"An isolated nucleotide sequence selecting from the group consisting of:

a) a nucleotide sequence encoding a maize polypeptide *having GDP-mannose pyrophosphorylase activity;*

b) a nucleotide sequence encoding the amino acid sequence of SEQ ID NO:2;

c) a nucleotide sequence set forth in SEQ ID NO:1; and

d) a nucleotide sequence having at least 90% identity to a nucleotide sequence of a), b), or c) *having GDP-mannose pyrophosphorylase activity.*"

GDP-mannose pyrophosphorylases comprise a well-characterized protein family that, at the time of filing, had been characterized at both the functional and structural level.

First, the structural characteristics of GDP-mannose pyrophosphorylase proteins were known in the art as discussed above. Moreover, Hashimoto, *et al.* page 16311, Fig 4, discloses the structural motifs common to members of this genus. Accordingly, Hashimoto *et al.* provide factual evidence that the structural elements required to structurally classify a polypeptide as a member of the GDP-mannose pyrophosphorylase polypeptide family was known in the art at the time the application was filed.

Second, the functional characteristics of the GDP-mannose pyrophosphorylase proteins were known in the art. Members of the GDP-mannose pyrophosphorylase protein family share a common function that was well characterized by the art at the time the application was filed. As indicated on page 4, lines 13-17 of the specification: "synthesis of the gum galactomannan is catalyzed by the enzymes mannan synthase and galactosyl transferase, from the substrates GDP-mannose and UDP-galactose. The formation of the substrate GDP-mannose, from mannose-1-phosphate and GTP, is catalyzed by the enzyme GDP-mannose pyrophosphorylase." The specification further provides functional assays that can be used to determined if a polypeptide has GDP-mannose pyrophosphorylase activity. See, for example, page 17, lines 29-30 of the specification. Hashimoto *et al.* apply similar assays to functionally characterize GDP-mannose pyrophosphorylase. Therefore, both the instant specification and Hshimoto *et al.* provide evidence that one of skill in the art, at the time the application was filed, was aware of the functional relationship that exists among the members of the GDP-mannose pyrophosphorylase protein family.

New independent claim 77 recites a nucleotide sequence encoding a maize polypeptide having GDP-mannose pyrophosphorylase activity, and a nucleotide sequence having at least 90% identity to a nucleotide sequence ... having GDP-mannose pyrophosphorylase activity. As discussed above, members of the GDP-mannose pyrophosphorylase protein family are well characterized both functionally and structurally. In addition, the recitation of 90% sequence identity is a *very*

predictable structure of the sequences encompassed by the claimed invention. As discussed above, the recitation of structural features common to the members of the genus is sufficient to satisfy the requirements of 35 U.S.C. §112, first paragraph.

It is further noted that new independent claim 77 recites that the claimed sequences encode a polypeptide that has GDP-mannose pyrophosphorylase activity upon expression in a plant or plant cell; thereby providing a functional characterization of the sequences claimed in the genus. Methods for assaying GDP-mannose pyrophosphorylase activity have been cited herein. Consequently, contrary to the Examiner's conclusions, the sequences encompassed by the current claims do not "include no description [of] the protein encoded by nucleic acids that have 90% identity to SEQ ID NO:1", but rather represent sequences having a well-defined structural and functional relationship.

Consequently, contrary to the Examiner's conclusion, the sequences encompassed by the genus of the present claims are defined by relevant identifying physical and chemical properties. In fact, the common attributes or features of the elements possessed by the members of the genus is that upon expression they have GDP-mannose pyrophosphorylase activity and share at least 90% sequence identity at the nucleotide level to the disclosed nucleotide sequence of SEQ ID NO:1. The requirement under 35 U.S.C. §112, first paragraph, as it relates to the present claims has been satisfied.

The Examiner states: "... the phenotype of plants transformed with antisense constructs of GDP-mannose pyrophosphorylase described in the specification on pg 3, lines 12-19, does not match the pheontype of plants transformed with antisense constructs of GDP-mannose pyrophosphorylase as described by Keller *et al*, as discussed above."

Keller *et al.* base their observations on only three clones selected for a virtual absence of GDP-mannose pyrophosphorylase activity (see response, herein). Keller *et al.* does not report the phenotype of plants expressing intermediate levels of enzyme activity that could well have demonstrated the phenotype described in the

specification. Thus, Keller *et al.* is not reliable as evidence that the specification does not provide written description for the present claims. However, to further prosecution and not to limit the scope of the claimed invention, new independent claim 77 has been written to omit the limitation of nucleic acids encoding antisense RNA.

The Examiner cites Regents of the University of California v. Eli Lilly and Co., 119 F.3d1559, 1569 (Fed. Cir. 1997) in support of the rejection. However, the Examiner has improperly applied this case to the present application. The decision in the Regents of the University of California turned on the conclusion that the patent lacked sufficient information "pertaining to the cDNA's relevant structure or physical characteristics." However, the decision did not exclude the possibility of claiming a genus of DNA molecules. In fact, a genus of DNAs may be described by means of a recitation of a representative number of DNAs, defined by nucleotide sequence, falling within the scope of the genus, or by means of a recitation of structural features common to the genus, which features constitute a substantial portion of the genus. Regents of the University of California v. Eli Lilly and Co., 119 F.3d1559, 1569 (Fed. Cir. 1997); see also Guidelines for Examination of Patent Applications Under the 35 U.S.C.112, first paragraph, "Written Description" Requirement, 66 Fed. Reg. 1099, 1106 (2000).

The Examiner's attention is drawn to the "Guidelines for the Examination of Patent Applications Under the 35 U.S.C 112, 1, 'Written Description' Requirement," which clearly state that "possession may be shown in many ways." 66 FR 1099, 1105. Applicants may satisfy the written description requirement by "disclosure of any combination of ... identifying characteristics that distinguish the claimed invention from other materials and would lead one of skill in the art to the conclusion that the applicant was in possession" of the invention. 66 FR 1099, 1106. Factors relevant to a determination of possession of a claimed invention include: "the level of skill and knowledge in the art, partial structure, physical and/or chemical properties, functional characteristics alone or coupled with known or disclosed correlation

between structure and function, and the method of making the claimed invention." 66 FR 1099, 1106.

Applicants have provided herein factual evidence that GDP-mannose pyrophosphorylase polypeptides, as recited in the present claims, comprise a well-characterized protein family that, at the time of filing, had been characterized at both the functional and structural level.

The Examiner concludes: "... the specification does not describe the sequence nucleic acid [sic] that encode legume GDP-mannose pyrophosphorylase or other maize GDP-mannose pyrophosphorylases. Additionally, the claims are not drawn to nucleic acids that have 90% identity to SEQ ID NO:1 and encode a GDP-mannose pyrophosphorylase, but are solely drawn to nucleic acids that have 90% sequence identity to SEQ ID NO:1. Lastly, description of the phenotype of plants transformed with antisense constructs of GDP-mannose pyrophosphorylase provided by the specification on pg 3, lines 12-19 does not match the phenotype of plants transformed with antisense constructs of GDP-mannose pyrophosphorylase described by Keller *et al*, as discussed above."

In summary, the Federal Circuit has made it clear that sufficient written description requires simply the knowledge and level of skill in the art to permit one of skill to immediately envision the product claimed from the disclosure. *Purdue Pharm L.P. v. Faulding In.*, 230 F.3d 1320 1323, 596 USPQ2d 1481, 1483 (Fed. Cir. 2000) ("One skilled in the art must immediately discern the limitations at issue in the claims."). As demonstrated above, the art was aware of both the structural and functional characteristics of GDP-mannose pyrophosphorylase proteins to distinguish these components of the claimed invention from other materials and therefore one of skill in the art would conclude that the applicant was in possession of the claimed species. The requirement under 35 U.S.C. §112, first paragraph, as it relates to the present claims has been satisfied.

Rejections under 35 USC §112, second paragraph:

Claims 3-4, 11, and 32-45 are rejected under §112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

The Examiner states: "Claim 3 lacks antecedent basis for the limitation 'said GDP-mannose' in line one.... Claims 4 and 8 lack antecedent basis for the limitation 'said leguminous plant' in line 1.... Claim 11 is not written in proper Markush format. The claims should be in the format 'selected from the group consisting of A, B, C, and D.' The phrase 'of promoters' should not be located after 'group of'.... In claim 32, --wherein– should be inserted before 'said' in line 3."

Claims 3, 4, 8, and 11 have been cancelled without prejudice. Claim 32 has been amended to incorporate the Examiner's suggestion. It is believed the cancellations and amendments obviate the rejections.

Rejections under 35 U.S.C. §103:

Claims 23, 32 and 41-45 are rejected under 35 U.S.C. §103(a) as being unpatentable over each of Gordon-Kamm *et al.* and Facciotti *et al.* in view of Hashimoto *et al.*, in further view of Wheeler *et al.*

The Examiner states: "The claims are drawn to plants and plant cells transformed with a nucleic acid encoding GDP-mannose pyrophosphorylase operably linked to a promoter.... At the time the invention was made, it would have been obvious to one of ordinary skill in the art to modify the method of plant transformation as taught by each of Gordon-Kamm *et al.* and Facciotti *et al.*, to transform plants with a nucleic acid encoding the GDP-mannose pyrophosphorylase described in Hashimoto *et al.* One of ordinary skill in the art would have been motivated to so because of the role GDP-mannose pyrophosphorylase in vitamin C biosynthesis (Wheeler *et al*, Figure 4) and to increase vitamin C content of plants."

Claims 23 and 32 have been amended.

It should be noted that it is clear that in order to establish a background for finding obviousness under 35 U.S. C. §103 that the determination of the scope and

contents of the prior art cannot be performed by the mere gathering of elements from separate and distinct disclosures irrespective of the teachings of the disclosures. There must be a reason apparent at the time the invention was made to select the particular combination or the references or the use of such teachings as evidence of obviousness will entail prohibited hindsight. *In re Nomiya*, 184 U.S.P.Q. 607 (CCPA 1975). No such motivation is present in the items cited by the Examiner, alone or in combination.

As noted by the Examiner, Gordon-Kamm *et al*, and Facciotti *et al* do not teach or disclose plants or plant cells transformed with the GDP- mannose pyrophosphorylase of the present invention.

Hashimoto *et al* does not teach the maize nucleic acid encoding GDP-mannose pyrophosphorylase of the present invention. The reference does not contain a teaching or suggestion for isolating a nucleic acid encoding GDP-mannose pyrophosphorylase from maize as claimed in the present invention.

Wheeler *et al* does not teach or suggest manipulation of the GDP- mannose pyrophosphorylase enzyme. In Figure 4 of Wheeler *et al* (cited by the Examiner), nine enzymes are describes acting in the "proposed pathway" (see last sentence of Wheeler *et al*). There is no teaching or suggestion which enzyme would be useful to regulate, nor whether up or down regulation should be targeted.

The Examiner is reminded that prior art itself must provide the skilled artisan the motivation to make the required substitution. In the present case, the Examiner has merely used Applicant's claims as a guide and selected secondary references that mention various aspects of the claimed invention. This is an improper standard. "One cannot use hindsight reconstruction to pick and choose among isolated disclosures in the prior art to deprecate the claimed invention." *In re Fine*, 837 F.2d 1071, 1075, 5 USPQ 2d 1596, 1600 (Fed. Cir. 1988). The law is clear that without motivation to combine the references, a rejection under 35 USC §103 fails.

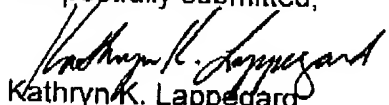
In summary, the Examiner has failed to establish a *prima facie* case of obviousness. As discussed above, there is not a sufficient motivation to combine

the teachings of Gordon-Kamm *et al.*, and Facciotti *et al.*, in view of Hashimoto *et al.*, in further view of Wheeler *et al.* to arrive at the claimed invention. Accordingly, Applicants respectfully submit that the claimed methods are not obvious in view of the cited references and respectfully request that the rejection of claims 23, 32 and 41-45 under 35 U.S.C. § 103(a) be withdrawn.

CONCLUSION

On the basis of the above amendments and remarks, reconsideration of the application and its allowance are respectfully requested.

Respectfully submitted,



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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the claims:

Claims 1, 3, 4, 7, 8, 11, 13, 24, and 33 have been cancelled without prejudice.

Claims 5, 23, 32 and 45 have been amended as follows:

5. (Amended) An expression cassette comprising a nucleotide sequence of claim 77 [1], wherein said nucleotide sequence is operably linked to a promoter that drives expression in a plant.

23. (Amended) A recombinant plant cell having stably incorporated into its genome at least one nucleotide sequence of claim 77 [encoding a GDP-mannose pyrophsphorylase or an antisense RNA thereof]; wherein said nucleotide sequence is operably linked to a promoter that drives expression in a plant.

32. (Amended) A transformed plant having stably incorporated into its genome at least one nucleotide sequence of claim 77 [encoding a GDP-mannose pyrophosphorylase or an antisense sequence thereof]; wherein said sequence is operably linked to a promoter that drives expression in a plant.

45. (Amended) The transformed seed of the plant of claim 32.

New claims 77-81 have been added as follows:

77. An isolated nucleotide sequence selecting from the group consisting of:

a) a nucleotide sequence encoding a maize polypeptide having GDP-mannose pyrophosphorylase activity;

b) a nucleotide sequence encoding the amino acid sequence of SEQ ID NO:2;

c) a nucleotide sequence set forth in SEQ ID NO:1; and

d) a nucleotide sequence having at least 90% identity to a nucleotide sequence of a), b), or c) having GDP-mannose pyrophosphorylase activity.

78. The isolated nucleotide sequence of claim 77 wherein the nucleotide sequence encodes a maize polypeptide having GDP-mannose pyrophosphorylase activity.

79. The isolated nucleotide sequence of claim 77 wherein the nucleotide sequence encodes the amino acid sequence of SEQ ID NO:2.

80. The isolated nucleotide sequence of claim 77 wherein the nucleotide sequence is set forth in SEQ ID NO:1.

81. The isolated nucleotide sequence of claim 77 wherein the nucleotide sequence has at least 90% identity to a nucleotide sequence of a), b), or c) having GDP-mannose pyrophosphorylase activity.